

*Development of an LC-MS Method for the Precise Quantification of TAGs in Biological Extracts*

Generally, precise quantification (RSD < 2%) using mass spectrometry requires the use of isotopically labeled internal standards. Compounds labeled with stable isotopes, such as  $^2\text{H}$ ,  $^{13}\text{C}$ , and  $^{15}\text{N}$  are generally expensive and selection is limited. Purchasing an array of labeled standards to support the quantitative analysis of multiple components in complex mixtures is prohibitively expensive at best. This project focuses on the development of a reverse-phase HPLC-MS method for the precise quantification of triglycerides (TAGs) in complex mixtures. The method will be based on a complex mixture of  $^{13}\text{C}$  labeled internal standards obtained via metabolic labeling of cultured yeast cells. Standard curves will be prepared for 30 different TAG species. These TAG species will be quantified in various extracts of vegetable oils, animal fats, and cultured cells. Relative molar sensitivities (RMS) of the 30 TAG species will be measured, and rules will be developed that can be used to predict RMS on the basis of fatty acid composition and position.